

64.00

#2



OIPE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/079,429

DATE: 03/08/2002 P.S

TIME: 14:32:43

Input Set : A:\106P3D1 SL Haseltine 021302 Human Genome Sciences.txt

Output Set: N:\CRF3\03082002\J079429.raw

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3 <110> APPLICANT: Haseltine et al.
5 <120> TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
7 <130> FILE REFERENCE: PF106P3D1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/079,429
10 <141> CURRENT FILING DATE: 2002-02-22
12 <150> PRIOR APPLICATION NUMBER: PCT/US95/01035
13 <151> PRIOR FILING DATE: 1995-01-25
15 <150> PRIOR APPLICATION NUMBER: 08/468,024
16 <151> PRIOR FILING DATE: 1995-06-06
18 <150> PRIOR APPLICATION NUMBER: 08/465,769
19 <151> PRIOR FILING DATE: 1995-06-06
21 <150> PRIOR APPLICATION NUMBER: 08/294,312
22 <151> PRIOR FILING DATE: 1994-08-23
24 <150> PRIOR APPLICATION NUMBER: 08/210,143
25 <151> PRIOR FILING DATE: 1994-03-16
27 <150> PRIOR APPLICATION NUMBER: 08/187,757
28 <151> PRIOR FILING DATE: 1994-01-27
30 <160> NUMBER OF SEQ ID NOS: 78
32 <170> SOFTWARE: PatentIn version 3.0
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35 <211> LENGTH: 2525
36 <212> TYPE: DNA
37 <213> ORGANISM: homo sapiens
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48 ggg gtt att cgg cgg ctg gac gag aca gtg gtg aac cgc atc gcg gcg      104
49 Gly Val Ile Arg Arg Leu Asp Glu Thr Val Val Asn Arg Ile Ala Ala
50           10           15           20
52 ggg gaa gtt atc cag cgg cca gct aat gct atc aaa gag atg att gag      152
53 Gly Glu Val Ile Gln Arg Pro Ala Asn Ala Ile Lys Glu Met Ile Glu
54           25           30           35
56 aac tgt tta gat gca aaa tcc aca agt att caa gtg att gtt aaa gag      200
57 Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln Val Ile Val Lys Glu
58           40           45           50
60 gga ggc ctg aag ttg att cag atc caa gac aat ggc acc ggg atc agg      248
61 Gly Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn Gly Thr Gly Ile Arg
62           55           60           65
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65 Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe Thr Thr Ser Lys Leu
66 70 75 80 85
68 cag tcc ttt gag gat tta gcc agt att tct acc tat ggc ttt cga ggt 344
69 Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr Tyr Gly Phe Arg Gly
70 90 95 100
72 gag gct ttg gcc agc ata agc cat gtg gct cat gtt act att aca acg 392
73 Glu Ala Leu Ala Ser Ile Ser His Val Ala His Val Thr Ile Thr Thr
74 105 110 115
76 aaa aca gct gat gga aag tgt gca tac aga gca agt tac tca gat gga 440
77 Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala Ser Tyr Ser Asp Gly
78 120 125 130
80 aaa ctg aaa gcc cct cct aaa cca tgt gct ggc aat caa ggg acc cag 488
81 Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly Asn Gln Gly Thr Gln
82 135 140 145
84 atc acg gtg gag gac ctt ttt tac aac ata gcc acg agg aga aaa gct 536
85 Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala Thr Arg Arg Lys Ala
86 150 155 160 165
88 tta aaa aat cca agt gaa gaa tat ggg aaa att ttg gaa gtt gtt ggc 584
89 Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile Leu Glu Val Val Gly
90 170 175 180
92 agg tat tca gta cac aat gca ggc att agt ttc tca gtt aaa aaa caa 632
93 Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe Ser Val Lys Lys Gln
94 185 190 195
96 gga gag aca gta gct gat gtt agg aca cta ccc aat gcc tca acc gtg 680
97 Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro Asn Ala Ser Thr Val
98 200 205 210
100 gac aat att cgc tcc gtc ttt gga aat gct gtt agt cga gaa ctg ata 728
101 Asp Asn Ile Arg Ser Val Phe Gly Asn Ala Val Ser Arg Glu Leu Ile
102 215 220 225
104 gaa att gga tgt gag gat aaa acc cta gcc ttc aaa atg aat ggt tac 776
105 Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe Lys Met Asn Gly Tyr
106 230 235 240 245
108 ata tcc aat gca aac tac tca gtg aag aag tgc atc ttc tta ctc ttc 824
109 Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys Ile Phe Leu Leu Phe
110 250 255 260
112 atc aac cat cgt ctg gta gaa tca act tcc ttg aga aaa gcc ata gaa 872
113 Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu Arg Lys Ala Ile Glu
114 265 270 275
116 aca gtg tat gca gcc tat ttg ccc aaa aac aca cac cca ttc ctg tac 920
117 Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr His Pro Phe Leu Tyr
118 280 285 290
120 ctc agt tta gaa atc agt ccc cag aat gtg gat gtt aat gtg cac ccc 968
121 Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp Val Asn Val His Pro
122 295 300 305
124 aca aag cat gaa gtt cac ttc ctg cac gag gag agc atc ctg gag cgg 1016
125 Thr Lys His Glu Val His Phe Leu His Glu Glu Ser Ile Leu Glu Arg
126 310 315 320 325
128 gtg cag cag cac atc gag agc aag ctc ctg ggc tcc aat tcc tcc agg 1064
129 Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly Ser Asn Ser Ser Arg
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Input Set : A:\106P3D1 SL Haseltine 021302 Human Genome Sciences.txt

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133	Met	Tyr	Phe	Thr	Gln	Thr	Leu	Leu	Pro	Gly	Leu	Ala	Gly	Pro	Ser	Gly	
134				345				350				355					
136	gag	atg	gtt	aaa	tcc	aca	aca	agt	ctg	acc	tcg	tct	tct	act	tct	gga	1160
137	Glu	Met	Val	Lys	Ser	Thr	Thr	Ser	Leu	Thr	Ser	Ser	Ser	Thr	Ser	Gly	
138				360				365				370					
140	agt	agt	gat	aag	gtc	tat	gcc	cac	cag	atg	gtt	cgt	aca	gat	tcc	cgg	1208
141	Ser	Ser	Asp	Lys	Val	Tyr	Ala	His	Gln	Met	Val	Arg	Thr	Asp	Ser	Arg	
142			375				380					385					
144	gaa	cag	aag	ctt	gat	gca	ttt	ctg	cag	cct	ctg	agc	aaa	ccc	ctg	tcc	1256
145	Glu	Gln	Lys	Leu	Asp	Ala	Phe	Leu	Gln	Pro	Leu	Ser	Lys	Pro	Leu	Ser	
146	390					395				400					405		
148	agt	cag	ccc	cag	gcc	att	gtc	aca	gag	gat	aag	aca	gat	att	tct	agt	1304
149	Ser	Gln	Pro	Gln	Ala	Ile	Val	Thr	Glu	Asp	Lys	Thr	Asp	Ile	Ser	Ser	
150				410				415				420					
152	ggc	agg	gct	agg	cag	caa	gat	gag	gag	atg	ctt	gaa	ctc	cca	gcc	cct	1352
153	Gly	Arg	Ala	Arg	Gln	Gln	Asp	Glu	Glu	Met	Leu	Glu	Leu	Pro	Ala	Pro	
154				425				430				435					
156	gct	gaa	gtg	gct	gcc	aaa	aat	cag	agc	ttg	gag	ggg	gat	aca	aca	aag	1400
157	Ala	Glu	Val	Ala	Ala	Lys	Asn	Gln	Ser	Leu	Glu	Gly	Asp	Thr	Thr	Lys	
158			440					445				450					
160	ggg	act	tca	gaa	atg	tca	gag	aag	aga	gga	cct	act	tcc	agc	aac	ccc	1448
161	Gly	Thr	Ser	Glu	Met	Ser	Glu	Lys	Arg	Gly	Pro	Thr	Ser	Ser	Asn	Pro	
162			455				460					465					
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165	Arg	Lys	Arg	His	Arg	Glu	Asp	Ser	Asp	Val	Glu	Met	Val	Glu	Asp	Asp	
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168	tcc	cga	aag	gaa	atg	act	gca	gct	tgt	acc	ccc	cgg	aga	agg	atc	att	1544
169	Ser	Arg	Lys	Glu	Met	Thr	Ala	Ala	Cys	Thr	Pro	Arg	Arg	Arg	Ile	Ile	
170				490				495				500					
172	aac	ctc	act	agt	gtt	ttg	agt	ctc	cag	gaa	gaa	att	aat	gag	cag	gga	1592
173	Asn	Leu	Thr	Ser	Val	Leu	Ser	Leu	Gln	Glu	Glu	Ile	Asn	Glu	Gln	Gly	
174				505				510				515					
176	cat	gag	gtt	ctc	cgg	gag	atg	ttg	cat	aac	cac	tcc	ttc	gtg	ggc	tgt	1640
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181	Val	Asn	Pro	Gln	Trp	Ala	Leu	Ala	Gln	His	Gln	Thr	Lys	Leu	Tyr	Leu	
182			535				540					545					
184	ctc	aac	acc	acc	aag	ctt	agt	gaa	gaa	ctg	ttc	tac	cag	ata	ctc	att	1736
185	Leu	Asn	Thr	Thr	Lys	Leu	Ser	Glu	Glu	Leu	Phe	Tyr	Gln	Ile	Leu	Ile	
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188	tat	gat	ttt	gcc	aat	ttt	ggt	gtt	ctc	agg	tta	tcg	gag	cca	gca	ccg	1784
189	Tyr	Asp	Phe	Ala	Asn	Phe	Gly	Val	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Pro	
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192	ctc	ttt	gac	ctt	gcc	atg	ctt	gcc	tta	gat	agt	cca	gag	agt	ggc	tgg	1832
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202      615      620      625
204 att gat gag gaa ggg aac ctg att gga tta ccc ctt ctg att gac aac      1976
205 Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro Leu Leu Ile Asp Asn
206 630      635      640      645
208 tat gtg ccc cct ttg gag gga ctg cct atc ttc att ctt cga cta gcc      2024
209 Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe Ile Leu Arg Leu Ala
210      650      655      660
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213 Thr Glu Val Asn Trp Asp Glu Glu Lys Glu Cys Phe Glu Ser Leu Ser
214      665      670      675
216 aaa gaa tgc gct atg ttc tat tcc atc cgg aag cag tac ata tct gag      2120
217 Lys Glu Cys Ala Met Phe Tyr Ser Ile Arg Lys Gln Tyr Ile Ser Glu
218      680      685      690
220 gag tcg acc ctc tca ggc cag cag agt gaa gtg cct ggc tcc att cca      2168
221 Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val Pro Gly Ser Ile Pro
222      695      700      705
224 aac tcc tgg aag tgg act gtg gaa cac att gtc tat aaa gcc ttg cgc      2216
225 Asn Ser Trp Lys Trp Thr Val Glu His Ile Val Tyr Lys Ala Leu Arg
226 710      715      720      725
228 tca cac att ctg cct cct aaa cat ttc aca gaa gat gga aat atc ctg      2264
229 Ser His Ile Leu Pro Pro Lys His Phe Thr Glu Asp Gly Asn Ile Leu
230      730      735      740
232 cag ctt gct aac ctg cct gat cta tac aaa gtc ttt gag agg tgt taa      2312
233 Gln Leu Ala Asn Leu Pro Asp Leu Tyr Lys Val Phe Glu Arg Cys
234      745      750      755
236 atatggttat ttatgcactg tgggatgtgt tcttctttct ctgtattccg atacaaagtg      2372
238 ttgtatcaaa gtgtgatata caaagtgtac caacataagt gttggttagca cttaagactt      2432
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261      35      40      45
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265      50      55      60
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281      115                    120                    125
284 Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly
285      130                    135                    140
288 Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala
289 145      150                    155                    160
292 Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile
293      165                    170                    175
296 Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe
297      180                    185                    190
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301      195                    200                    205
304 Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Val Phe Gly Asn Ala Val
305      210                    215                    220
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309 225      230                    235                    240
312 Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys
313      245                    250                    255
316 Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu
317      260                    265                    270
320 Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr
321      275                    280                    285
324 His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp
325      290                    295                    300
328 Val Asn Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu
329 305      310                    315                    320
332 Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly
333      325                    330                    335
336 Ser Asn Ser Ser Arg Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu
337      340                    345                    350
340 Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser
341      355                    360                    365
344 Ser Ser Thr Ser Gly Ser Ser Asp Lys Val Tyr Ala His Gln Met Val
345      370                    375                    380
348 Arg Thr Asp Ser Arg Glu Gln Lys Leu Asp Ala Phe Leu Gln Pro Leu
349 385      390                    395                    400
352 Ser Lys Pro Leu Ser Ser Gln Pro Gln Ala Ile Val Thr Glu Asp Lys
353      405                    410                    415
356 Thr Asp Ile Ser Ser Gly Arg Ala Arg Gln Gln Asp Glu Glu Met Leu
357      420                    425                    430
360 Glu Leu Pro Ala Pro Ala Glu Val Ala Ala Lys Asn Gln Ser Leu Glu
361      435                    440                    445
364 Gly Asp Thr Thr Lys Gly Thr Ser Glu Met Ser Glu Lys Arg Gly Pro
365      450                    455                    460
368 Thr Ser Ser Asn Pro Arg Lys Arg His Arg Glu Asp Ser Asp Val Glu
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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:1537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17